The metabolome of induced pluripotent stem cells reveals metabolic changes occurring in somatic cell reprogramming.

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Public Summary:
Metabolism is vital to every aspect of cell function, yet the metabolome of induced pluripotent stem cells (iPSCs) remains largely unexplored. Here we report, using an untargeted metabolomics approach, that human iPSCs share a pluripotent metabolomic signature with embryonic stem cells (ESCs) that is distinct from their parental cells, and that is characterized by changes in metabolites involved in cellular respiration. Examination of cellular bioenergetics corroborated with our metabolomic analysis, and demonstrated that somatic cells convert from an oxidative state to a glycolytic state in pluripotency. Interestingly, the bioenergetics of various somatic cells correlated with their reprogramming efficiencies. We further identified metabolites that differ between iPSCs and ESCs, which revealed novel metabolic pathways that play a critical role in regulating somatic cell reprogramming. Our findings are the first to globally analyze the metabolome of iPSCs, and provide mechanistic insight into a new layer of regulation involved in inducing pluripotency, and in evaluating iPSC and ESC equivalence.

Scientific Abstract:
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